AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1-73. (canceled)

74. (new) A method of modulating in a catharanthus plant cell the level(s) of one or more terpenoid indole alkaloids (TIAs), and/or of modulating the expression of one or more nucleic acids responsible for the biosynthesis of a TIA or a precursor thereof, said method comprising providing to the cell an AP2-domain transcription factor comprising at least one AP2-domain having an amino acid sequence with at least 90% amino acid identity with SEQ ID NO:6.

75. (new) The method according to claim 74, wherein the AP2-domain transcription factor is provided to the cell by the expression in said cell, under the control of an expression regulating sequence operable in said cell, of a nucleotide sequence that encodes the AP2-domain transcription factor.

76. (new) The method according to claim 75, comprising the steps of:

(a) transforming the cell with a nucleic acid construct, said construct comprising the nucleotide sequence encoding the AP2-domain transcription factor, operably linked to said expression regulating sequence;

(b) maintaining the cell under conditions such that the nucleotide sequence is expressed in said cell.

77. (new) The method according to claim 75, wherein the expression regulating sequence is heterologous to the cell and/or in which the expression regulating sequence is an expression regulating sequence with which the nucleotide sequence that encodes the AP2-domain transcription factor is not natively associated.

78. (new) The method according to claim 74, wherein the plant cell is *Catharanthus roseus*.

79. (new) The method according to claim 74, wherein the TIA is selected from the group consisting of serpentine, ajmalicine, vincristine, vinblastine, camptothecine, quinine, quinidine, reserpine, strictosidine, rescinnamine, ellipticine and precursors and/or intermediates therefore.

80. (new) The method according to claim 74, wherein the nucleic acid involved in the biosynthesis of the TIA encodes a protein or polypeptide, including but not limited to an enzyme.

81. (new) The method according to claim 80 wherein the enzymes are selected from the group consisting of: Tdc, Str, Cpr, D4h, Asa and Dxs.

82. (new) An isolated nucleic acid molecule comprising a nucleotide sequence selected from:

(a) SEQ ID NO: 3;

(b) a nucleotide sequence encoding an AP2-domain transcription factor having at least one AP2-domain and having an amino acid sequence with at least 90% amino acid identity with SEQ ID NO:6.

83. (new) The isolated nucleic acid molecule according to claim 82, wherein said sequence comprises SEQ ID NO:3.

84. (new) The isolated nucleic acid according to claim 82, wherein the AP2-domain comprises SEQ ID NO:6.

85. (new) The method according to claim 74, wherein the AP2-domain comprises SEQ ID NO:6.

86. (new) The method according to claim 74, further comprising:

transforming the cell with a nucleic acid construct, said construct comprising the nucleotide sequence SEQ ID NO:3;

maintaining the cell under conditions such that the nucleotide sequence is expressed in said cell and encodes an AP2-domain transcription factor comprising SEQ ID NO:6; and

wherein said plant cell is from a plant selected from the group of species consisting of C. roseus, C. coriaceus, C. lanceus, C. longifolius, C. ovalis, C. pusillus, and C. trichophyllus; and wherein said (TIAs) are selected from the group consisting of serpentine, ajmalicine, vincristine, vinblastine, camptothecine, quinine, quinidine, reserpine, strictosidine, rescinnamine, ellipticine and precursors and/or intermediates therefore.

87. (new) A method of modulating in a *Catharanthus roseus* plant cell the level(s) of AP2-domain transcription factor, said method comprising transforming said cell with a nucleic acid construct comprising at least one nucleotide sequence encoding an AP-2 domain transcription factor, wherein said nucleotide sequence is operably linked to an expression regulating sequence;

maintaining said cell such that the level of AP2-domain transcription factor is expressed;

and wherein said AP2 transcription factor comprising an amino acid sequence having at least 90% homology with SEQ ID NO:6.

88. (new) The method according to claim 87, wherein the AP2-domain comprises SEQ ID NO:6.